

INS
C 2

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: KEESEE, SUSAN
OBAR, ROBERT
WU, YING-JYE

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
DETECTION OF CERVICAL CANCER

(iii) NUMBER OF SEQUENCES: 46

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Testa, Hurwitz & Thibeault
(B) STREET: 125 High St.
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: GREENHALGH, DUNCAN A
(B) REGISTRATION NUMBER: 38,678
(C) REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 248-7000
(B) TELEFAX: (617) 248-7100

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Pro Ala Ala Ser Leu Ala Val His Thr Asp Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Phe Ser Gly Gln Ile Glu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg Leu Ile Ala Glu Ala Lys Glu Lys
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro Ser Leu Val His Ser Arg Asp Met
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Trp Asp Ile Ser Thr Val Ser Ser Val Asn Glu Ala Phe Gly Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Val Leu Gly Ser Ala Arg Asn Ser Ser Ile Ser Gly Pro Phe Gly
1 5 10 15
Ser Arg

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Asp Lys Pro Ile Phe Thr Leu Asn Ala His Asn Asp Glu Ile Ser
1 5 10 15
Gly Leu Asp Leu Ser Ser Gln Ile Lys
20 25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Gln Thr Leu Gln Phe His Pro Phe Glu Ala Gln Thr Leu Ile Ser
1 5 10 15
Gly Ser Tyr Asp Lys
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Val Leu Phe Cys Ser Ser Cys Cys Pro Asp Leu Pro Phe Ile
1 5 10 15

Tyr Ala Phe Gly Gly Gln Lys
20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asn Arg Ser Arg Gln Val Thr Cys Val Ala Trp Val Arg Cys Gly
1 5 10 15

Val Ala Lys Glu Thr Pro Asp Lys Val Glu Leu Ser Lys Glu Glu Val
20 25 30

Lys Arg Leu Ile Ala Glu Ala Lys Glu Lys Leu Gln Glu Gly Gly
35 40 45

Gly Ser Asp Glu Glu Glu Thr Gly Ser Pro Ser Glu Asp Gly Met Gln
50 55 60

Ser Ala Arg Thr Gln Ala Arg Pro Arg Glu Pro Leu Glu Asp Gly Asp
65 70 75 80

Pro Glu Asp Asp Arg Thr Leu Asp Asp Asp Glu Leu Ala Glu Tyr Asp
85 90 95

Leu Asp Lys Tyr Asp Glu Glu Gly Asp Pro Asp Ala Glu Thr Leu Gly
100 105 110

Glu Ser Leu Leu Gly Leu Thr Val Tyr Gly Ser Asn Asp Gln Asp Pro
115 120 125

Tyr Val Thr Leu Lys Asp Thr Glu Gln Tyr Glu Arg Glu Asp Phe Leu
130 135 140

Ile Lys Pro Ser Asp Asn Leu Ile Val Cys Gly Arg Ala Glu Gln Asp
145 150 155 160

Gln Cys Asn Leu Glu Val His Val Tyr Asn Gln Glu Glu Asp Ser Phe
165 170 175

Tyr Val His His Asp Ile Leu Leu Ser Ala Tyr Pro Leu Ser Val Glu
180 185 190

Trp Leu Asn Phe Asp Pro Ser Pro Asp Asp Ser Thr Gly Asn Tyr Ile
195 200 205

Ala Val Gly Asn Met Thr Pro Val Ile Glu Val Trp Asp Leu Asp Ile
210 215 220

Val Asp Ser Leu Glu Pro Val Phe Thr Leu Gly Ser Lys Leu Ser Lys
225 230 235 240

Lys Lys Lys Lys Lys Gly Lys Lys Ser Ser Ser Ala Glu Gly His Thr
 245 250 255
 5 Asp Ala Val Leu Asp Leu Ser Trp Asn Lys Leu Ile Arg Asn Val Leu
 260 265 270
 Ala Ser Ala Ser Ala Asp Asn Thr Val Ile Leu Trp Asp Met Ser Leu
 275 280 285
 10 Gly Lys Pro Ala Ala Ser Leu Ala Val His Thr Asp Lys Val Gln Thr
 290 295 300
 Leu Gln Phe His Pro Phe Glu Ala Gln Thr Leu Ile Ser Gly Ser Tyr
 305 310 315 320
 15 Asp Lys Ser Val Ala Leu Tyr Asp Cys Arg Ser Pro Asp Glu Ser His
 325 330 335
 Arg Met Trp Arg Phe Ser Gly Gln Ile Glu Arg Val Thr Trp Asn His
 340 345 350
 Phe Ser Pro Cys His Phe Leu Ala Ser Thr Asp Asp Gly Phe Val Tyr
 355 360 365
 25 Asn Leu Asp Ala Arg Ser Asp Lys Pro Ile Phe Thr Leu Asn Ala His
 370 375 380
 Asn Asp Glu Ile Ser Gly Leu Asp Leu Ser Ser Gln Ile Lys Gly Cys
 385 390 395 400
 30 Leu Val Thr Ala Ser Ala Asp Lys Tyr Val Lys Ile Trp Asp Ile Leu
 405 410 415
 Gly Asp Arg Pro Ser Leu Val His Ser Arg Asp Met Lys Met Gly Val
 420 425 430
 35 Leu Phe Cys Ser Ser Cys Cys Pro Asp Leu Pro Phe Ile Tyr Ala Phe
 435 440 445
 Gly Gly Gln Lys Glu Gly Leu Arg Val Trp Asp Ile Ser Thr Val Ser
 450 455 460
 40 Ser Val Asn Glu Ala Phe Gly Arg Arg Glu Arg Leu Val Leu Gly Ser
 465 470 475 480
 45 Ala Arg Asn Ser Ser Ile Ser Gly Pro Phe Gly Ser Arg Ser Ser Asp
 485 490 495
 50 Thr Pro Met Glu Ser
 500

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asp Tyr Ser Gln Tyr Tyr Arg
1 5

5 (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn His Glu Glu Glu Met Asn Ala Leu Arg
1 5 10

20 (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Leu Glu Gly Glu Asp Ala His Leu Thr Gln Tyr Lys
1 5 10

35 (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Leu Asn Glu Met Arg
1 5

50 (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser Glu Ile Ser Glu Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asp Ala Glu Asp Trp Phe Phe Ser Lys
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Ser Val Glu Ala Asp Ile Asn Gly Leu Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Thr Thr Ser Ile Arg Gln Phe Thr Ser Ser Ser Ser Ile Lys Gly
1 5 10 15

Ser Ser Gly Leu Gly Gly Gly Ser Ser Arg Thr Ser Cys Arg Leu Ser
20 25 30

Gly Gly Leu Gly Ala Gly Ser Cys Arg Leu Gly Ser Ala Gly Gly Leu
35 40 45

Gly Ser Thr Leu Gly Gly Ser Ser Tyr Ser Ser Cys Tyr Ser Phe Gly
50 55 60

Ser Gly Gly Gly Tyr Gly Ser Ser Phe Gly Gly Val Asp Gly Leu Leu
65 70 75 80

Ala Gly Gly Glu Lys Ala Thr Met Gln Asn Leu Asn Asp Arg Leu Ala
85 90 95

	Ser	Tyr	Leu	Asp	Lys	Val	Arg	Ala	Leu	Glu	Glu	Ala	Asn	Thr	Glu	Leu
				100					105					110		
5	Glu	Val	Lys	Ile	Arg	Asp	Trp	Tyr	Gln	Arg	Gln	Ala	Pro	Gly	Pro	Ala
			115					120					125			
	Arg	Asp	Tyr	Ser	Gln	Tyr	Tyr	Arg	Thr	Ile	Glu	Glu	Leu	Gln	Asn	Lys
		130					135					140				
10	Ile	Leu	Thr	Ala	Thr	Val	Asp	Asn	Ala	Asn	Ile	Leu	Leu	Gln	Ile	Asp
	145					150					155				160	
	Asn	Ala	Arg	Leu	Ala	Ala	Asp	Asp	Phe	Arg	Thr	Lys	Phe	Glu	Thr	Glu
				165					170						175	
15	Gln	Ala	Leu	Arg	Leu	Ser	Val	Glu	Ala	Asp	Ile	Asn	Gly	Leu	Arg	Arg
				180					185					190		
20	Val	Leu	Asp	Glu	Leu	Thr	Leu	Ala	Arg	Ala	Asp	Leu	Glu	Met	Gln	Ile
			195					200					205			
	Glu	Asn	Leu	Lys	Glu	Glu	Leu	Ala	Tyr	Leu	Lys	Lys	Asn	His	Glu	Glu
		210					215					220				
25	Glu	Met	Asn	Ala	Leu	Arg	Gly	Gln	Val	Gly	Gly	Glu	Ile	Asn	Val	Glu
	225					230					235					240
	Met	Asp	Ala	Ala	Pro	Gly	Val	Asp	Leu	Ser	Arg	Ile	Leu	Asn	Glu	Met
					245				250						255	
30	Arg	Asp	Gln	Tyr	Glu	Lys	Met	Ala	Glu	Lys	Asn	Arg	Lys	Asp	Ala	Glu
				260					265					270		
35	Asp	Trp	Phe	Phe	Ser	Lys	Thr	Glu	Glu	Leu	Asn	Arg	Glu	Val	Ala	Thr
			275					280					285			
	Asn	Ser	Glu	Leu	Val	Gln	Ser	Gly	Lys	Ser	Glu	Ile	Ser	Glu	Leu	Arg
		290					295					300				
40	Arg	Thr	Met	Gln	Ala	Leu	Glu	Ile	Glu	Leu	Gln	Ser	Gln	Leu	Ser	Met
	305					310					315				320	
	Lys	Ala	Ser	Leu	Glu	Gly	Asn	Leu	Ala	Glu	Thr	Glu	Asn	Arg	Tyr	Cys
				325						330					335	
45	Val	Gln	Leu	Ser	Gln	Ile	Gln	Gly	Leu	Ile	Gly	Ser	Val	Glu	Glu	Gln
				340					345					350		
50	Leu	Ala	Gln	Leu	Arg	Cys	Glu	Met	Glu	Gln	Gln	Asn	Gln	Glu	Tyr	Lys
			355					360					365			
	Ile	Leu	Leu	Asp	Val	Lys	Thr	Arg	Leu	Glu	Gln	Glu	Ile	Ala	Thr	Tyr
		370					375					380				
55	Arg	Arg	Leu	Leu	Glu	Gly	Glu	Asp	Ala	His	Leu	Thr	Gln	Tyr	Lys	Lys
	385					390					395				400	
	Glu	Pro	Val	Thr	Thr	Arg	Gln	Val	Arg	Thr	Ile	Val	Glu	Glu	Val	Gln
					405					410					415	
60	Asp	Gly	Lys	Val	Ile	Ser	Ser	Arg	Glu	Gln	Val	His	Gln	Thr	Thr	Arg
				420					425					430		

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Phe Gly Gly Asn Pro Gly Gly Phe Gly Asn Gln Gly Gly Phe Gly Asn
1 5 10 15
Ser Arg

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Trp Cys Asp Cys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Thr Thr Glu Gln Asp Leu Lys
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Phe Gly Phe Val Arg
1 5

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu Pro Asn Ser Lys Gln Ser Gln Asp Glu Pro Leu Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Lys Met Asp Glu Thr Asp Ala Ser Ser Ala Val Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Thr Ser Asp Leu Ile Val Leu Gly Leu Pro Trp Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ser Glu Tyr Ile Arg Val Thr Glu Asp Glu Asn Asp Glu Pro Ile
1 5 10 15

Glu Ile Pro Ser Glu Asp Asp Gly Thr Val Leu Leu Ser Thr Val Thr
 20 25 30
 5 Ala Gln Phe Pro Gly Ala Cys Gly Leu Arg Tyr Arg Asn Pro Val Ser
 35 40 45
 Gln Cys Met Arg Gly Val Arg Leu Val Glu Gly Ile Leu His Ala Pro
 50 55 60
 10 Asp Ala Gly Trp Gly Asn Leu Val Tyr Val Val Asn Tyr Pro Lys Asp
 65 70 75 80
 Asn Lys Arg Lys Met Asp Glu Thr Asp Ala Ser Ser Ala Val Lys Val
 85 90 95
 15 Lys Arg Ala Val Gln Lys Thr Ser Asp Leu Ile Val Leu Gly Leu Pro
 100 105 110
 20 Trp Lys Thr Thr Glu Gln Asp Leu Lys Glu Tyr Phe Ser Thr Phe Gly
 115 120 125
 Glu Val Leu Met Val Gln Val Lys Lys Asp Leu Lys Thr Gly His Ser
 130 135 140
 25 Lys Gly Phe Gly Phe Val Arg Phe Thr Glu Tyr Glu Thr Gln Val Lys
 145 150 155 160
 Val Met Ser Gln Arg His Met Ile Asp Gly Arg Trp Cys Asp Cys Lys
 165 170 175
 30 Leu Pro Asn Ser Lys Gln Ser Gln Asp Glu Pro Leu Arg Ser Arg Lys
 180 185 190
 35 Val Phe Val Gly Arg Cys Thr Glu Asp Met Thr Glu Asp Glu Leu Arg
 195 200 205
 Glu Phe Phe Ser Gln Tyr Gly Asp Val Met Asp Val Phe Ile Pro Lys
 210 215 220
 40 Pro Phe Arg Ala Phe Ala Phe Val Thr Phe Ala Asp Asp Gln Ile Ala
 225 230 235 240
 Gln Ser Leu Cys Gly Glu Asp Leu Ile Ile Lys Gly Ile Ser Val His
 245 250 255
 45 Ile Ser Asn Ala Glu Pro Lys His Asn Ser Asn Arg Gln Leu Glu Arg
 260 265 270
 50 Ser Gly Arg Phe Gly Gly Asn Pro Gly Gly Phe Gly Asn Gln Gly Gly
 275 280 285
 Phe Gly Asn Ser Arg Gly Gly Gly Ala Gly Leu Gly Asn Asn Gln Gly
 290 295 300
 55 Ser Asn Met Gly Gly Gly Met Asn Phe Gly Ala Phe Ser Ile Asn Pro
 305 310 315 320
 Ala Met Met Ala Ala Ala Gln Ala Ala Leu Gln Ser Ser Trp Gly Met
 325 330 335
 60 Met Gly Met Leu Ala Ser Gln Gln Asn Gln Ser Gly Pro Ser Gly Asn
 340 345 350
 65 Asn Gln Asn Gln Gly Asn Met Gln Arg Glu Pro Asn Gln Ala Phe Gly
 355 360 365

Ser Gly Asn Asn Ser Tyr Ser Gly Ser Asn Ser Gly Ala Ala Ile Gly
370 375 380

Trp Gly Ser Ala Ser Asn Ala Gly Ser Gly Ser Gly Phe Asn Gly Gly
385 390 395 400

Phe Gly Ser Ser Met Asp Ser Lys Ser Ser Gly Trp Gly Met
405 410

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Asn Tyr Tyr Arg
1

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asn Tyr Tyr Arg
1

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Val Gln Glu Ala Gln Lys
1 5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Glu Val Ala Asp Cys Phe Lys
1 5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

His Asp Gly Thr Gly Gly Gln Ser Ile Tyr Gly Asp Lys Phe Glu Asp
1 5 10 15

Glu Asn Phe Asp Val Lys
20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ile Thr Met Glu Leu Phe Xaa Asn Ile Val Pro Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

His Thr Gly Pro Gly Leu Leu Ser Met Ala Asn Gln Gly Gln Asn Thr
1 5 10 15

Asn Asn Xaa Xaa Phe Val Ile Xaa Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3224 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Arg Arg Ser Lys Ala Asp Val Glu Arg Tyr Ile Ala Ser Val Gln
1 5 10 15
Gly Ser Thr Pro Ser Pro Arg Gln Lys Ser Met Lys Gly Phe Tyr Phe
20 25 30
Ala Lys Leu Tyr Tyr Glu Ala Lys Glu Tyr Asp Leu Ala Lys Lys Tyr
35 40 45
Ile Cys Thr Tyr Ile Asn Val Gln Glu Arg Asp Pro Lys Ala His Arg
50 55 60
Phe Leu Gly Leu Leu Tyr Glu Leu Glu Glu Asn Thr Asp Lys Ala Val
65 70 75 80
Glu Cys Tyr Arg Arg Ser Val Glu Leu Asn Pro Thr Gln Lys Asp Leu
85 90 95
Val Leu Lys Ile Ala Glu Leu Leu Cys Lys Asn Asp Val Thr Asp Gly
100 105 110
Arg Ala Lys Tyr Trp Leu Glu Arg Ala Ala Lys Leu Phe Pro Gly Ser
115 120 125
Pro Ala Ile Tyr Lys Leu Lys Glu Gln Leu Leu Asp Cys Glu Gly Glu
130 135 140
Asp Gly Trp Asn Lys Leu Phe Asp Leu Ile Gln Ser Glu Leu Tyr Val
145 150 155 160
Arg Pro Asp Asp Val His Val Asn Ile Arg Leu Val Glu Val Tyr Arg
165 170 175
Ser Thr Lys Arg Leu Lys Asp Ala Val Ala His Cys His Glu Ala Glu
180 185 190
Arg Asn Ile Ala Leu Arg Ser Ser Leu Glu Trp Asn Ser Cys Val Val
195 200 205
Gln Thr Leu Lys Glu Tyr Leu Glu Ser Leu Gln Cys Leu Glu Ser Asp
210 215 220
Lys Ser Asp Trp Arg Ala Thr Asn Thr Asp Leu Leu Leu Ala Tyr Ala
225 230 235 240
Asn Leu Met Leu Leu Thr Leu Ser Thr Arg Asp Val Gln Glu Ser Arg
245 250 255
Glu Leu Leu Gln Ser Phe Asp Ser Ala Leu Gln Ser Val Lys Ser Leu
260 265 270
Gly Gly Asn Asp Glu Leu Ser Ala Thr Phe Leu Glu Met Lys Gly His
275 280 285

	Phe	Tyr	Met	His	Ala	Gly	Ser	Leu	Leu	Leu	Lys	Met	Gly	Gln	His	Ser
	290						295				300					
5	Ser	Asn	Val	Gln	Trp	Arg	Ala	Leu	Ser	Glu	Leu	Ala	Ala	Leu	Cys	Tyr
	305					310				315					320	
	Leu	Ile	Ala	Phe	Gln	Val	Pro	Arg	Pro	Lys	Ile	Lys	Leu	Ile	Lys	Gly
10					325					330					335	
	Glu	Ala	Gly	Gln	Asn	Leu	Leu	Glu	Met	Met	Ala	Cys	Asp	Arg	Leu	Ser
				340					345					350		
15	Gln	Ser	Gly	His	Met	Leu	Leu	Asn	Leu	Ser	Arg	Gly	Lys	Gln	Asp	Phe
			355					360					365			
	Leu	Lys	Glu	Ile	Val	Glu	Thr	Phe	Ala	Asn	Lys	Ser	Gly	Gln	Ser	Ala
	370						375					380				
20	Leu	Tyr	Asp	Ala	Leu	Phe	Ser	Ser	Gln	Ser	Pro	Lys	Asp	Thr	Ser	Phe
	385					390					395					400
	Leu	Gly	Ser	Asp	Asp	Ile	Gly	Asn	Ile	Asp	Val	Arg	Glu	Pro	Glu	Leu
				405						410					415	
25	Glu	Asp	Leu	Thr	Arg	Tyr	Asp	Val	Gly	Ala	Ile	Arg	Ala	His	Asn	Gly
				420					425					430		
30	Ser	Leu	Gln	His	Leu	Thr	Trp	Leu	Gly	Leu	Gln	Trp	Asn	Ser	Leu	Pro
		435					440						445			
	Ala	Leu	Pro	Gly	Ile	Arg	Lys	Trp	Leu	Lys	Gln	Leu	Phe	His	His	Leu
	450						455					460				
35	Pro	His	Glu	Thr	Ser	Arg	Leu	Glu	Thr	Asn	Ala	Pro	Glu	Ser	Ile	Cys
	465					470					475					480
	Ile	Leu	Asp	Leu	Glu	Val	Phe	Leu	Leu	Gly	Val	Val	Tyr	Thr	Ser	His
				485						490					495	
40	Leu	Gln	Leu	Lys	Glu	Lys	Cys	Asn	Ser	His	His	Ser	Ser	Tyr	Gln	Pro
			500						505					510		
45	Leu	Cys	Leu	Pro	Leu	Pro	Val	Cys	Lys	Gln	Leu	Cys	Thr	Glu	Arg	Gln
		515					520						525			
	Lys	Ser	Trp	Trp	Asp	Ala	Val	Cys	Thr	Leu	Ile	His	Arg	Lys	Ala	Val
		530					535					540				
50	Pro	Gly	Asn	Val	Ala	Lys	Leu	Arg	Leu	Leu	Val	Gln	His	Glu	Ile	Asn
	545					550					555					560
	Thr	Leu	Arg	Ala	Gln	Glu	Lys	His	Gly	Leu	Gln	Pro	Ala	Leu	Leu	Val
				565					570						575	
55	His	Trp	Ala	Glu	Cys	Leu	Gln	Lys	Thr	Gly	Ser	Gly	Leu	Asn	Ser	Phe
			580						585					590		
60	Tyr	Asp	Gln	Arg	Glu	Tyr	Ile	Gly	Arg	Ser	Val	His	Tyr	Trp	Lys	Lys
			595					600					605			
	Val	Leu	Pro	Leu	Leu	Lys	Ile	Ile	Lys	Lys	Lys	Asn	Ser	Ile	Pro	Glu
		610					615					620				

	Pro	Ile	Asp	Pro	Leu	Phe	Lys	His	Phe	His	Ser	Val	Asp	Ile	Gln	Ala	625	630	635	640
5	Ser	Glu	Ile	Val	Glu	Tyr	Glu	Glu	Asp	Ala	His	Ile	Thr	Phe	Ala	Ile	645	650	655	
	Leu	Asp	Ala	Val	Asn	Gly	Asn	Ile	Glu	Asp	Ala	Val	Thr	Ala	Phe	Glu	660	665	670	
10	Ser	Ile	Lys	Ser	Val	Val	Ser	Tyr	Trp	Asn	Leu	Ala	Leu	Ile	Phe	His	675	680	685	
	Arg	Lys	Ala	Glu	Asp	Ile	Glu	Asn	Asp	Ala	Leu	Ser	Pro	Glu	Glu	Gln	690	695	700	
15	Glu	Glu	Cys	Lys	Asn	Tyr	Leu	Arg	Lys	Thr	Arg	Asp	Tyr	Leu	Ile	Lys	705	710	715	720
	Ile	Ile	Asp	Asp	Ser	Asp	Ser	Asn	Leu	Ser	Val	Val	Lys	Lys	Leu	Pro	725	730	735	
20	Val	Pro	Leu	Glu	Ser	Val	Lys	Glu	Met	Leu	Asn	Ser	Val	Met	Gln	Glu	740	745	750	
25	Leu	Glu	Asp	Tyr	Ser	Glu	Gly	Gly	Pro	Leu	Tyr	Lys	Asn	Gly	Ser	Leu	755	760	765	
	Arg	Asn	Ala	Asp	Ser	Glu	Ile	Lys	Arg	Ser	Thr	Pro	Ser	Pro	Thr	Arg	770	775	780	
30	Tyr	Ser	Leu	Ser	Pro	Ser	Lys	Ser	Tyr	Lys	Tyr	Ser	Pro	Lys	Thr	Pro	785	790	795	800
	Pro	Arg	Trp	Ala	Glu	Asp	Gln	Asn	Ser	Leu	Leu	Lys	Met	Ile	Cys	Gln	805	810	815	
35	Gln	Val	Glu	Ala	Ile	Lys	Lys	Glu	Met	Gln	Glu	Leu	Lys	Leu	Asn	Ser	820	825	830	
40	Ser	Asn	Ser	Ala	Ser	Pro	His	Arg	Trp	Pro	Thr	Glu	Asn	Tyr	Gly	Pro	835	840	845	
	Asp	Ser	Val	Pro	Asp	Gly	Tyr	Gln	Gly	Ser	Gln	Thr	Phe	His	Gly	Ala	850	855	860	
45	Pro	Leu	Thr	Val	Ala	Thr	Thr	Gly	Pro	Ser	Val	Tyr	Tyr	Ser	Gln	Ser	865	870	875	880
	Pro	Ala	Tyr	Asn	Ser	Gln	Tyr	Leu	Leu	Arg	Pro	Ala	Ala	Asn	Val	Thr	885	890	895	
50	Pro	Thr	Lys	Gly	Pro	Val	Tyr	Gly	Met	Asn	Arg	Leu	Pro	Pro	Gln	Gln	900	905	910	
55	His	Ile	Tyr	Ala	Tyr	Pro	Gln	Gln	Met	His	Thr	Pro	Pro	Val	Gln	Ser	915	920	925	
	Ser	Ser	Ala	Cys	Met	Phe	Ser	Gln	Glu	Met	Tyr	Gly	Pro	Pro	Ala	Leu	930	935	940	
60	Arg	Phe	Glu	Ser	Pro	Ala	Thr	Gly	Ile	Leu	Ser	Pro	Arg	Gly	Asp	Asp	945	950	955	960
65	Tyr	Phe	Asn	Tyr	Asn	Val	Gln	Gln	Thr	Ser	Thr	Asn	Pro	Pro	Leu	Pro	965	970	975	

	Ala Met	Ala Ser	Asn Gln	Ala Val	Arg Ile	Val Lys	Glu Pro	Thr Ser	
	1315			1320			1325		
5	His Asp	Asn Lys	Asp Ile	Cys Lys	Ser Asp	Ala Gly	Asn Leu	Asn Phe	
	1330			1335		1340			
	Glu Phe	Gln Val	Ala Lys	Lys Glu	Gly Ser	Trp Trp	His Cys	Asn Ser	
	1345		1350			1355		1360	
10	Cys Ser	Leu Lys	Asn Ala	Ser Thr	Ala Lys	Lys Cys	Val Ser	Cys Gln	
			1365		1370			1375	
	Asn Leu	Asn Pro	Ser Asn	Lys Glu	Leu Val	Gly Pro	Pro Leu	Ala Glu	
15			1380		1385			1390	
	Thr Val	Phe Thr	Pro Lys	Thr Ser	Pro Glu	Asn Val	Gln Asp	Arg Phe	
		1395		1400			1405		
20	Ala Leu	Val Thr	Pro Lys	Lys Glu	Gly His	Trp Asp	Cys Ser	Ile Cys	
	1410			1415		1420			
	Leu Val	Arg Asn	Glu Pro	Thr Val	Ser Arg	Cys Ile	Ala Cys	Gln Asn	
	1425		1430			1435		1440	
25	Thr Lys	Ser Ala	Asn Lys	Ser Gly	Ser Ser	Phe Val	His Gln	Ala Ser	
			1445			1450		1455	
	Phe Lys	Phe Gly	Gln Gly	Asp Leu	Pro Lys	Pro Ile	Asn Ser	Asp Phe	
30			1460		1465			1470	
	Arg Ser	Val Phe	Ser Thr	Lys Glu	Gly Gln	Trp Asp	Cys Ser	Ala Cys	
		1475		1480			1485		
35	Leu Val	Gln Asn	Glu Gly	Ser Ser	Thr Lys	Cys Ala	Ala Cys	Gln Asn	
	1490			1495		1500			
	Pro Arg	Lys Gln	Ser Leu	Pro Ala	Thr Ser	Ile Pro	Thr Pro	Ala Ser	
	1505		1510			1515		1520	
40	Phe Lys	Phe Gly	Thr Ser	Glu Thr	Ser Lys	Thr Leu	Lys Ser	Gly Phe	
			1525			1530		1535	
	Glu Asp	Met Phe	Ala Lys	Lys Glu	Gly Gln	Trp Asp	Cys Ser	Ser Cys	
45			1540		1545			1550	
	Leu Val	Arg Asn	Glu Ala	Asn Ala	Thr Arg	Cys Val	Ala Cys	Gln Asn	
		1555		1560			1565		
50	Pro Asp	Lys Pro	Ser Pro	Ser Thr	Ser Val	Pro Ala	Pro Ala	Ser Phe	
		1570		1575		1580			
	Lys Phe	Gly Thr	Ser Glu	Thr Ser	Lys Ala	Pro Lys	Ser Gly	Phe Glu	
	1585		1590			1595		1600	
55	Gly Met	Phe Thr	Lys Lys	Glu Gly	Gln Trp	Asp Cys	Ser Val	Cys Leu	
			1605		1610			1615	
	Val Arg	Asn Glu	Ala Ser	Ala Thr	Lys Cys	Ile Ala	Cys Gln	Asn Pro	
60			1620		1625			1630	
	Gly Lys	Gln Asn	Gln Thr	Thr Ser	Ala Val	Ser Thr	Pro Ala	Ser Ser	
		1635		1640			1645		
65	Glu Thr	Ser Lys	Ala Pro	Lys Ser	Gly Phe	Glu Gly	Met Phe	Thr Lys	
	1650			1655		1660			

Lys Glu Gly Gln Trp Asp Cys Ser Val Cys Leu Val Arg Asn Glu Ala
 1665 1670 1675 1680
 5 Ser Ala Thr Lys Cys Ile Ala Cys Gln Asn Pro Gly Lys Gln Asn Gln
 1685 1690 1695
 Thr Thr Ser Ala Val Ser Thr Pro Ala Ser Ser Glu Thr Ser Lys Ala
 1700 1705 1710
 10 Pro Lys Ser Gly Phe Glu Gly Met Phe Thr Lys Lys Glu Gly Gln Trp
 1715 1720 1725
 Asp Cys Ser Val Cys Leu Val Arg Asn Glu Ala Ser Ala Thr Lys Cys
 1730 1735 1740
 15 Ile Ala Cys Gln Cys Pro Ser Lys Gln Asn Gln Thr Thr Ala Ile Ser
 1745 1750 1755 1760
 20 Thr Pro Ala Ser Ser Glu Ile Ser Lys Ala Pro Lys Ser Gly Phe Glu
 1765 1770 1775
 Gly Met Phe Ile Arg Lys Gly Gln Trp Asp Cys Ser Val Cys Cys Val
 1780 1785 1790
 25 Gln Asn Glu Ser Ser Ser Leu Lys Cys Val Ala Cys Asp Ala Ser Lys
 1795 1800 1805
 Pro Thr His Lys Pro Ile Ala Glu Ala Pro Ser Ala Phe Thr Leu Gly
 1810 1815 1820
 30 Ser Glu Met Lys Leu His Asp Ser Ser Gly Ser Gln Val Gly Thr Gly
 1825 1830 1835 1840
 Phe Lys Ser Asn Phe Ser Glu Lys Ala Ser Lys Phe Gly Asn Thr Glu
 1845 1850 1855
 35 Gln Gly Phe Lys Phe Gly His Val Asp Gln Glu Asn Ser Pro Ser Phe
 1860 1865 1870
 40 Met Phe Gln Gly Ser Ser Asn Thr Glu Phe Lys Ser Thr Lys Glu Gly
 1875 1880 1885
 Phe Ser Ile Pro Val Ser Ala Asp Gly Phe Lys Phe Gly Ile Ser Glu
 1890 1895 1900
 45 Pro Gly Asn Gln Glu Lys Lys Ser Glu Lys Pro Leu Glu Asn Gly Thr
 1905 1910 1915 1920
 50 Gly Phe Gln Ala Gln Asp Ile Ser Gly Gln Lys Asn Gly Arg Gly Val
 1925 1930 1935
 Ile Phe Gly Gln Thr Ser Ser Thr Phe Thr Phe Ala Asp Leu Ala Lys
 1940 1945 1950
 55 Ser Thr Ser Gly Glu Gly Phe Gln Phe Gly Lys Lys Asp Pro Asn Phe
 1955 1960 1965
 Lys Gly Phe Ser Gly Ala Gly Glu Lys Leu Phe Ser Ser Gln Tyr Gly
 1970 1975 1980
 60 Lys Met Ala Asn Lys Ala Asn Thr Ser Gly Asp Phe Glu Lys Asp Asp
 1985 1990 1995 2000
 65

Asp Ala Tyr Lys Thr Glu Asp Ser Asp Asp Ile His Phe Glu Pro Val
 2005 2010 2015
 5 Val Gln Met Pro Glu Lys Val Glu Leu Val Thr Gly Glu Glu Asp Glu
 2020 2025 2030
 Lys Val Leu Tyr Ser Gln Arg Val Lys Leu Phe Arg Phe Asp Ala Glu
 2035 2040 2045
 10 Val Ser Gln Trp Lys Glu Arg Gly Leu Gly Asn Leu Lys Ile Leu Lys
 2050 2055 2060
 Asn Glu Val Asn Gly Lys Leu Arg Met Leu Met Arg Arg Glu Gln Val
 2065 2070 2075 2080
 15 Leu Lys Val Cys Ala Asn His Trp Ile Thr Thr Thr Met Asn Leu Lys
 2085 2090 2095
 Pro Leu Ser Gly Ser Asp Arg Ala Trp Met Trp Leu Ala Ser Asp Phe
 2100 2105 2110
 Ser Asp Gly Asp Ala Lys Leu Glu Gln Leu Ala Ala Lys Phe Lys Thr
 2115 2120 2125
 25 Pro Glu Leu Ala Glu Glu Phe Lys Gln Lys Phe Glu Glu Cys Gln Arg
 2130 2135 2140
 Leu Leu Leu Asp Ile Pro Leu Gln Thr Pro His Lys Leu Val Asp Thr
 2145 2150 2155 2160
 30 Gly Arg Ala Ala Lys Leu Ile Gln Arg Ala Glu Glu Met Lys Ser Gly
 2165 2170 2175
 Leu Lys Asp Phe Lys Thr Phe Leu Thr Asn Asp Gln Thr Lys Val Thr
 2180 2185 2190
 35 Glu Glu Glu Asn Lys Gly Ser Gly Thr Gly Ala Ala Gly Ala Ser Asp
 2195 2200 2205
 Thr Thr Ile Lys Pro Asn Pro Glu Asn Thr Gly Pro Thr Leu Glu Trp
 2210 2215 2220
 40 Asp Asn Tyr Asp Leu Arg Glu Asp Ala Leu Asp Asp Ser Val Ser Ser
 2225 2230 2235 2240
 Ser Ser Val His Ala Ser Pro Leu Ala Ser Ser Pro Val Arg Lys Asn
 2245 2250 2255
 50 Leu Phe Arg Phe Gly Glu Ser Thr Thr Gly Phe Asn Phe Ser Phe Lys
 2260 2265 2270
 Ser Ala Leu Ser Pro Ser Lys Ser Pro Ala Lys Leu Asn Gln Ser Gly
 2275 2280 2285
 55 Thr Ser Val Gly Thr Asp Glu Glu Ser Asp Val Thr Gln Glu Glu Glu
 2290 2295 2300
 Arg Asp Gly Gln Tyr Phe Glu Pro Val Val Pro Leu Pro Asp Leu Val
 2305 2310 2315 2320
 60 Glu Val Ser Ser Gly Glu Glu Asn Glu Gln Val Val Phe Ser His Arg
 2325 2330 2335
 Ala Lys Leu Tyr Arg Tyr Asp Lys Asp Val Gly Gln Trp Lys Glu Arg
 2340 2345 2350
 65

Gly Ile Gly Asp Ile Lys Ile Leu Gln Asn Tyr Asp Asn Lys Gln Val
 2355 2360 2365
 5 Arg Ile Val Met Arg Arg Asp Gln Val Leu Lys Leu Cys Ala Asn His
 2370 2375 2380
 10 Arg Ile Thr Pro Asp Met Thr Leu Gln Asn Met Lys Gly Thr Glu Arg
 2385 2390 2395 2400
 Val Trp Leu Trp Thr Ala Cys Asp Phe Ala Asp Gly Glu Arg Lys Val
 2405 2410 2415
 15 Glu His Leu Ala Val Arg Phe Lys Leu Gln Asp Val Ala Asp Ser Phe
 2420 2425 2430
 Lys Lys Ile Phe Asp Glu Ala Lys Thr Ala Gln Glu Lys Asp Ser Leu
 2435 2440 2445
 20 Ile Thr Pro His Val Ser Arg Ser Ser Thr Pro Arg Glu Ser Pro Cys
 2450 2455 2460
 Gly Lys Ile Ala Val Ala Val Leu Glu Glu Thr Thr Arg Glu Arg Thr
 2465 2470 2475 2480
 25 Asp Val Ile Gln Gly Asp Asp Val Ala Asp Ala Thr Ser Glu Val Glu
 2485 2490 2495
 Val Ser Ser Thr Ser Glu Thr Thr Pro Lys Ala Val Val Ser Pro Pro
 2500 2505 2510
 30 Lys Phe Val Phe Gly Ser Glu Ser Val Lys Ser Ile Phe Ser Ser Glu
 2515 2520 2525
 35 Lys Ser Lys Pro Phe Ala Phe Gly Asn Ser Ser Ala Thr Gly Ser Leu
 2530 2535 2540
 Phe Gly Phe Ser Phe Asn Ala Pro Leu Lys Ser Asn Asn Ser Glu Thr
 2545 2550 2555 2560
 40 Ser Ser Val Ala Gln Ser Gly Ser Glu Ser Lys Val Glu Pro Lys Lys
 2565 2570 2575
 45 Cys Glu Leu Ser Lys Asn Ser Asp Ile Glu Gln Ser Ser Asp Ser Lys
 2580 2585 2590
 Val Lys Asn Leu Phe Ala Ser Phe Pro Thr Glu Glu Ser Ser Ile Asn
 2595 2600 2605
 50 Tyr Thr Phe Lys Thr Pro Glu Lys Ala Lys Glu Lys Lys Lys Pro Glu
 2610 2615 2620
 Asp Ser Pro Ser Asp Asp Asp Val Leu Ile Val Tyr Glu Leu Thr Pro
 2625 2630 2635 2640
 55 Thr Ala Glu Gln Lys Ala Leu Ala Thr Lys Leu Lys Leu Pro Pro Thr
 2645 2650 2655
 Phe Phe Cys Tyr Lys Asn Arg Pro Asp Tyr Val Ser Glu Glu Glu Glu
 2660 2665 2670
 60 Asp Asp Glu Asp Phe Glu Thr Ala Val Lys Lys Leu Asn Gly Lys Leu
 2675 2680 2685
 65

	Tyr	Leu	Asp	Gly	Ser	Glu	Lys	Cys	Arg	Pro	Leu	Glu	Glu	Asn	Thr	Ala	
	2690						2695					2700					
5	Asp	Asn	Glu	Lys	Glu	Cys	Ile	Ile	Val	Trp	Glu	Lys	Lys	Pro	Thr	Val	
	2705					2710					2715					2720	
	Glu	Glu	Lys	Ala	Lys	Ala	Asp	Thr	Leu	Lys	Leu	Pro	Pro	Thr	Phe	Phe	
					2725					2730						2735	
10	Cys	Gly	Val	Cys	Ser	Asp	Thr	Asp	Glu	Asp	Asn	Gly	Asn	Gly	Glu	Asp	
				2740					2745					2750			
	Phe	Gln	Ser	Glu	Leu	Gln	Lys	Val	Gln	Glu	Ala	Gln	Lys	Ser	Gln	Thr	
			2755				2760							2765			
15	Glu	Glu	Ile	Thr	Ser	Thr	Thr	Asp	Ser	Val	Tyr	Thr	Gly	Gly	Thr	Glu	
			2770				2775						2780				
	Val	Met	Val	Pro	Ser	Phe	Cys	Lys	Ser	Glu	Glu	Pro	Asp	Ser	Ile	Thr	
20	2785						2790					2795				2800	
	Lys	Ser	Ile	Ser	Ser	Pro	Ser	Val	Ser	Ser	Glu	Thr	Met	Asp	Lys	Pro	
						2805					2810				2815		
25	Val	Asp	Leu	Ser	Thr	Arg	Lys	Glu	Ile	Asp	Thr	Asp	Ser	Thr	Ser	Gln	
				2820					2825						2830		
	Gly	Glu	Ser	Lys	Ile	Val	Ser	Phe	Gly	Phe	Gly	Ser	Ser	Thr	Gly	Leu	
			2835					2840						2845			
30	Ser	Phe	Ala	Asp	Leu	Ala	Ser	Ser	Asn	Ser	Gly	Asp	Phe	Ala	Phe	Gly	
		2850					2855					2860					
	Ser	Lys	Asp	Lys	Asn	Phe	Gln	Trp	Ala	Asn	Thr	Gly	Ala	Ala	Val	Phe	
35	2865					2870					2875					2880	
	Gly	Thr	Gln	Ser	Val	Gly	Thr	Gln	Ser	Ala	Gly	Lys	Val	Gly	Glu	Asp	
					2885					2890					2895		
40	Glu	Asp	Gly	Ser	Asp	Glu	Glu	Val	Val	His	Asn	Glu	Asp	Ile	His	Phe	
				2900						2905					2910		
	Glu	Pro	Ile	Val	Ser	Leu	Pro	Glu	Val	Glu	Val	Lys	Ser	Gly	Glu	Glu	
			2915					2920						2925			
45	Asp	Glu	Glu	Ile	Leu	Phe	Lys	Glu	Arg	Ala	Lys	Leu	Tyr	Arg	Trp	Asp	
		2930					2935						2940				
	Arg	Asp	Val	Ser	Gln	Trp	Lys	Glu	Arg	Gly	Val	Gly	Asp	Ile	Lys	Ile	
50	2945					2950					2955					2960	
	Leu	Trp	His	Thr	Met	Lys	Asn	Tyr	Tyr	Arg	Ile	Leu	Met	Arg	Arg	Asp	
					2965					2970					2975		
55	Gln	Val	Phe	Lys	Val	Cys	Ala	Asn	His	Val	Ile	Thr	Lys	Thr	Met	Glu	
					2980				2985						2990		
	Leu	Lys	Pro	Leu	Asn	Val	Ser	Asn	Asn	Ala	Leu	Val	Trp	Thr	Ala	Ser	
			2995					3000					3005				
60	Asp	Tyr	Ala	Asp	Gly	Glu	Ala	Lys	Val	Glu	Gln	Leu	Ala	Val	Arg	Phe	
		3010					3015						3020				
	Lys	Thr	Lys	Glu	Val	Ala	Asp	Cys	Phe	Lys	Lys	Thr	Phe	Glu	Glu	Cys	
65	3025					3030					3035					3040	

Gln Gln Asn Leu Met Lys Leu Gln Lys Gly His Val Ser Leu Ala Ala
3045 3050 3055

5 Glu Leu Ser Lys Glu Thr Asn Pro Val Val Phe Phe Asp Val Cys Ala
3060 3065 3070

10 Asp Gly Glu Pro Leu Gly Arg Ile Thr Met Glu Leu Phe Ser Asn Ile
3075 3080 3085

15 Val Pro Arg Thr Ala Glu Asn Phe Arg Ala Leu Cys Thr Gly Glu Lys
3090 3095 3100

Gly Phe Gly Phe Lys Asn Ser Ile Phe His Arg Val Ile Pro Asp Phe
3105 3110 3115 3120

20 Val Cys Gln Gly Gly Asp Ile Thr Lys His Asp Gly Thr Gly Gly Gln
3125 3130 3135

Ser Ile Tyr Gly Asp Lys Phe Glu Asp Glu Asn Phe Asp Val Lys His
3140 3145 3150

25 Thr Gly Pro Gly Leu Leu Ser Met Ala Asn Gln Gly Gln Asn Thr Asn
3155 3160 3165

Asn Ser Gln Phe Val Ile Thr Leu Lys Lys Ala Glu His Leu Asp Phe
3170 3175 3180

30 Lys His Val Val Phe Gly Phe Val Lys Asp Gly Met Asp Thr Val Lys
3185 3190 3195 3200

Lys Ile Glu Ser Phe Gly Ser Pro Lys Gly Ser Val Cys Arg Arg Ile
3205 3210 3215

35 Thr Ile Thr Glu Cys Gly Gln Ile
3220

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Phe Glu Ser Arg
1 5

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Thr Tyr Ser Ala Lys
1 5

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Asp Asn Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Thr Tyr Ser Ala Lys
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Asn Ile Tyr Ser Glu Glu Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Thr Ala Leu Ser Glu Lys Arg
1 5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Leu Ala Leu Asp Met Glu Ile His Ala Tyr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Glu Met Ala Glu Met Arg Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Glu Glu Leu Asp Phe Gln Lys Asn Ile Tyr Ser Glu Glu Leu Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Glu Glu Leu Asp Phe Gln Lys Asn Ile Tyr Ser Glu Glu Leu Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 515 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly Glu Leu His Asp Leu
1 5 10 15

Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu Gly Glu Ala Lys Lys
20 25 30

Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp Ala Glu Asn Arg Leu
35 40 45

Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys Asn Ile Tyr Ser Glu
50 55 60

Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr Arg Leu Val Glu Ile
65 70 75 80

Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg Leu Ala Asp Ala Leu
85 90 95

Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val Glu Gln Tyr Lys Lys
100 105 110

Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp Asn Ala Arg Gln Ser
115 120 125

Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala His Glu Glu Leu Gln
130 135 140

Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala Gln Leu Ser Gln Leu
145 150 155 160

	Gln	Lys	Gln	Leu	Ala	Ala	Lys	Glu	Ala	Lys	Leu	Arg	Asp	Leu	Glu	Asp	
					165					170					175		
5	Ser	Leu	Ala	Arg	Glu	Arg	Asp	Thr	Ser	Arg	Arg	Leu	Leu	Ala	Glu	Lys	
				180					185					190			
	Glu	Arg	Glu	Met	Ala	Glu	Met	Arg	Ala	Arg	Met	Gln	Gln	Gln	Leu	Asp	
			195					200					205				
10	Glu	Tyr	Gln	Glu	Leu	Leu	Asp	Ile	Lys	Leu	Ala	Leu	Asp	Met	Glu	Ile	
		210					215					220					
	His	Ala	Tyr	Arg	Lys	Leu	Leu	Glu	Gly	Glu	Glu	Glu	Arg	Leu	Arg	Leu	
15		225				230				235						240	
	Ser	Pro	Ser	Pro	Thr	Ser	Gln	Arg	Ser	Arg	Gly	Arg	Ala	Ser	Ser	His	
					245				250						255		
20	Ser	Ser	Gln	Thr	Gln	Gly	Gly	Gly	Ser	Val	Thr	Lys	Lys	Arg	Lys	Leu	
				260					265					270			
	Glu	Ser	Thr	Glu	Ser	Arg	Ser	Ser	Phe	Ser	Gln	His	Ala	Arg	Thr	Ser	
			275					280					285				
25	Gly	Arg	Val	Ala	Val	Glu	Glu	Val	Asp	Glu	Glu	Gly	Lys	Phe	Val	Arg	
		290					295					300					
	Leu	Arg	Asn	Lys	Ser	Asn	Glu	Asp	Gln	Ser	Met	Gly	Asn	Trp	Gln	Ile	
30		305				310					315					320	
	Lys	Arg	Gln	Asn	Gly	Asp	Asp	Pro	Leu	Leu	Thr	Tyr	Arg	Phe	Pro	Pro	
				325					330					335			
35	Lys	Phe	Thr	Leu	Lys	Ala	Gly	Gln	Val	Val	Thr	Ile	Trp	Ala	Ala	Gly	
				340				345						350			
	Ala	Gly	Ala	Thr	His	Ser	Pro	Pro	Thr	Asp	Leu	Val	Trp	Lys	Ala	Gln	
			355				360						365				
40	Asn	Thr	Trp	Gly	Cys	Gly	Asn	Ser	Leu	Arg	Thr	Ala	Leu	Ile	Asn	Ser	
		370					375					380					
	Thr	Gly	Glu	Glu	Val	Ala	Met	Arg	Lys	Leu	Val	Arg	Ser	Val	Thr	Val	
45		385				390					395					400	
	Val	Glu	Asp	Asp	Glu	Asp	Glu	Asp	Gly	Asp	Asp	Leu	Leu	His	His	His	
				405					410					415			
50	His	Gly	Ser	His	Cys	Ser	Ser	Ser	Gly	Asp	Pro	Ala	Glu	Tyr	Asn	Leu	
			420						425					430			
	Arg	Ser	Arg	Thr	Val	Leu	Cys	Gly	Thr	Cys	Gly	Gln	Pro	Ala	Asp	Lys	
			435					440					445				
55	Ala	Ser	Ala	Ser	Gly	Ser	Gly	Ala	Gln	Val	Gly	Gly	Pro	Ile	Ser	Ser	
		450					455					460					
	Gly	Ser	Ser	Ala	Ser	Ser	Val	Thr	Val	Thr	Arg	Ser	Tyr	Arg	Ser	Val	
60		465					470				475					480	
	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Phe	Gly	Asp	Asn	Leu	Val	Thr	Arg	Ser	
				485					490						495		
65	Tyr	Leu	Leu	Gly	Asn	Ser	Ser	Pro	Arg	Thr	Gln	Ser	Pro	Gln	Asn	Cys	
			500						505					510			

Ser Ile Met
515

667650" 667650" 667650"